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RAW SEQUENCE LISTING

DATE: 01/10/2002

PATENT APPLICATION: US/10/020,733

TIME: 15:52:03

Input Set : A:\LEX-0263-USA SEQLIST.txt

Output Set: N:\CRF3\01102002\J020733.raw

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4 <110> APPLICANT: Walke, D. Wade
5   Wilganowski, Nathaniel L.
6   Friddle, Carl Johan
9 <120> TITLE OF INVENTION: Novel Human Proteases and Polynucleotides Encoding the Same
11 <130> FILE REFERENCE: LEX-0263-USA
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/020,733
C--> 13 <141> CURRENT FILING DATE: 2001-10-30
13 <150> PRIOR APPLICATION NUMBER: US 60/244,939
14 <151> PRIOR FILING DATE: 2000-11-01
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22 <212> TYPE: DNA
23 <213> ORGANISM: homo sapiens
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28 ctgcagcatg aaacttatcat acctcagtgg aagacttcag aaagccccgt gagagaaaag      180
29 catccactca aagctgagct cagggtaatg gctgaggggc gagaactgat cctggacctg      240
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37 ttagagtttc agaagaatcg acgagaccag gacgccacca aacacaagct catagagatc      720
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42 tctgtgtacc agtctggagg agtcaacatg gaccactccg agaatgccat tggcgtggct      1020
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59 catggggtct gtaacaacaa ccagaactgc cactgcctgc cgggctgggc ccgccccttc 2040
60 tgcaacacac cgggccacgg gggcagtatc gacagtgggc ctatgcccc tgagagtgtg 2100
61 ggtcctgtgg tagctggagt gttggtggcc atcttgggtg tggcggctct catgctgatg 2160
62 tactactgct gcagacagaa caacaaacta ggccaaactc agccctcagc tctcccttcc 2220
63 aagctgaggg aacagttcag ttgtcccttc agggtttctc agaacagcgg gactgggtcat 2280
64 gccaacccaa ctttcaagct gcagacgccc cagggaagc gaaagggtgt ccttgacttg 2340
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69 tccaggctc gccgccccca gaaggcactc ccggcaaac cagtgccagg ccgcaggagc 2640
70 ctccccaggc caggaggtgc atccccactg cggccccctg gtgctggccc tcagcagtc 2700
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74 <210> SEQ ID NO: 2

75 <211> LENGTH: 926

76 <212> TYPE: PRT

77 <213> ORGANISM: homo sapiens

79 <400> SEQUENCE: 2

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81 1 5 10 15
82 Leu Gln Pro Leu Arg Pro Arg Ala Ala Arg Glu Pro Gly Trp Thr Arg
83 20 25 30
84 Gly Ser Glu Glu Gly Ser Pro Lys Leu Gln His Glu Leu Ile Ile Pro
85 35 40 45
86 Gln Trp Lys Thr Ser Glu Ser Pro Val Arg Glu Lys His Pro Leu Lys
87 50 55 60
88 Ala Glu Leu Arg Val Met Ala Glu Gly Arg Glu Leu Ile Leu Asp Leu
89 65 70 75 80
90 Glu Lys Asn Glu Gln Leu Phe Ala Pro Ser Tyr Thr Glu Thr His Tyr
91 85 90 95
92 Thr Ser Ser Gly Asn Pro Gln Thr Thr Thr Arg Lys Leu Glu Asp His
93 100 105 110
94 Cys Phe Tyr His Gly Thr Val Arg Glu Thr Glu Leu Ser Ser Val Thr
95 115 120 125
96 Leu Ser Thr Cys Arg Gly Ile Arg Gly Leu Ile Thr Val Ser Ser Asn
97 130 135 140
98 Leu Ser Tyr Val Ile Glu Pro Leu Pro Asp Ser Lys Gly Gln His Leu
99 145 150 155 160
100 Ile Tyr Arg Ser Glu His Leu Lys Pro Pro Gly Asn Cys Gly Phe
101 165 170 175
102 Glu His Ser Lys Pro Thr Thr Arg Asp Trp Ala Leu Gln Phe Thr Gln
103 180 185 190
104 Gln Thr Lys Lys Arg Pro Arg Arg Met Lys Arg Glu Asp Leu Asn Ser
105 195 200 205
106 Met Lys Tyr Val Glu Leu Tyr Leu Val Ala Asp Tyr Leu Glu Phe Gln
107 210 215 220

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108 Lys Asn Arg Arg Asp Gln Asp Ala Thr Lys His Lys Leu Ile Glu Ile
109 225                230                235                240
110 Ala Asn Tyr Val Asp Lys Phe Tyr Arg Ser Leu Asn Ile Arg Ile Ala
111                245                250                255
112 Leu Val Gly Leu Glu Val Trp Thr His Gly Asn Met Cys Glu Val Ser
113                260                265                270
114 Glu Asn Pro Tyr Ser Thr Leu Trp Ser Phe Leu Ser Trp Arg Arg Lys
115                275                280                285
116 Leu Leu Ala Gln Lys Tyr His Asp Asn Ala Gln Leu Ile Thr Gly Met
117                290                295                300
118 Ser Phe His Gly Thr Thr Ile Gly Leu Ala Pro Leu Met Ala Met Cys
119 305                310                315                320
120 Ser Val Tyr Gln Ser Gly Gly Val Asn Met Asp His Ser Glu Asn Ala
121                325                330                335
122 Ile Gly Val Ala Ala Thr Met Ala His Glu Met Gly His Asn Phe Gly
123                340                345                350
124 Met Thr His Asp Ser Ala Asp Cys Cys Ser Ala Ser Ala Ala Asp Gly
125                355                360                365
126 Gly Cys Ile Met Ala Ala Ala Thr Gly His Pro Phe Pro Lys Val Phe
127                370                375                380
128 Asn Gly Cys Asn Arg Arg Glu Leu Asp Arg Tyr Leu Gln Ser Gly Gly
129 385                390                395                400
130 Gly Met Cys Leu Ser Asn Met Pro Asp Thr Arg Met Leu Tyr Gly Gly
131                405                410                415
132 Arg Arg Cys Gly Asn Gly Tyr Leu Glu Asp Gly Glu Glu Cys Asp Cys
133                420                425                430
134 Gly Glu Glu Glu Glu Cys Asn Asn Pro Cys Cys Asn Ala Ser Asn Cys
135                435                440                445
136 Thr Leu Arg Pro Gly Ala Glu Cys Ala His Gly Ser Cys Cys His Gln
137                450                455                460
138 Cys Lys Leu Leu Ala Pro Gly Thr Leu Cys Arg Glu Gln Ala Arg Gln
139 465                470                475                480
140 Cys Asp Leu Pro Glu Phe Cys Thr Gly Lys Ser Pro His Cys Pro Thr
141                485                490                495
142 Asn Phe Tyr Gln Met Asp Gly Thr Pro Cys Glu Gly Gly Gln Ala Tyr
143                500                505                510
144 Cys Tyr Asn Gly Met Cys Leu Thr Tyr Gln Glu Gln Cys Gln Gln Leu
145                515                520                525
146 Trp Gly Pro Gly Ala Arg Pro Ala Pro Asp Leu Cys Phe Glu Lys Val
147                530                535                540
148 Asn Val Ala Gly Asp Thr Phe Gly Asn Cys Gly Lys Asp Met Asn Gly
149 545                550                555                560
150 Glu His Arg Lys Cys Asn Met Arg Asp Ala Lys Cys Gly Lys Ile Gln
151                565                570                575
152 Cys Gln Ser Ser Glu Ala Arg Pro Leu Glu Ser Asn Ala Val Pro Ile
153                580                585                590
154 Asp Thr Thr Ile Ile Met Asn Gly Arg Gln Ile Gln Cys Arg Gly Thr
155                595                600                605
156 His Val Tyr Arg Gly Pro Glu Glu Glu Gly Asp Met Leu Asp Pro Gly

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157      610      615      620
158 Leu Val Met Thr Gly Thr Lys Cys Gly Tyr Asn His Ile Cys Phe Glu
159 625      630      635      640
160 Gly Gln Cys Arg Asn Thr Ser Phe Phe Glu Thr Glu Gly Cys Gly Lys
161      645      650      655
162 Lys Cys Asn Gly His Gly Val Cys Asn Asn Asn Gln Asn Cys His Cys
163      660      665      670
164 Leu Pro Gly Trp Ala Pro Pro Phe Cys Asn Thr Pro Gly His Gly Gly
165      675      680      685
166 Ser Ile Asp Ser Gly Pro Met Pro Pro Glu Ser Val Gly Pro Val Val
167      690      695      700
168 Ala Gly Val Leu Val Ala Ile Leu Val Leu Ala Val Leu Met Leu Met
169 705      710      715      720
170 Tyr Tyr Cys Cys Arg Gln Asn Asn Lys Leu Gly Gln Leu Lys Pro Ser
171      725      730      735
172 Ala Leu Pro Ser Lys Leu Arg Gln Gln Phe Ser Cys Pro Phe Arg Val
173      740      745      750
174 Ser Gln Asn Ser Gly Thr Gly His Ala Asn Pro Thr Phe Lys Leu Gln
175      755      760      765
176 Thr Pro Gln Gly Lys Arg Lys Val Phe Leu Asp Leu Cys Val Gln Val
177      770      775      780
178 Ile Asn Thr Pro Glu Ile Leu Arg Lys Pro Ser Gln Pro Pro Pro Arg
179 785      790      795      800
180 Pro Pro Pro Asp Tyr Leu Arg Gly Gly Ser Pro Pro Ala Pro Leu Pro
181      805      810      815
182 Ala His Leu Ser Arg Ala Ala Arg Asn Ser Pro Gly Pro Gly Ser Gln
183      820      825      830
184 Ile Glu Arg Thr Glu Ser Ser Arg Arg Pro Pro Pro Ser Arg Pro Ile
185      835      840      845
186 Pro Pro Ala Pro Asn Cys Ile Val Ser Gln Asp Phe Ser Arg Pro Arg
187      850      855      860
188 Pro Pro Gln Lys Ala Leu Pro Ala Asn Pro Val Pro Gly Arg Arg Ser
189 865      870      875      880
190 Leu Pro Arg Pro Gly Gly Ala Ser Pro Leu Arg Pro Pro Gly Ala Gly
191      885      890      895
192 Pro Gln Gln Ser Arg Pro Leu Ala Ala Leu Ala Pro Lys Arg Val Trp
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195      915      920      925
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198 <211> LENGTH: 2757
199 <212> TYPE: DNA
200 <213> ORGANISM: homo sapiens
202 <400> SEQUENCE: 3
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205 ctgcagcatg aacttatcat acctcagtgg aagacttcag aaagccccgt gagagaaaag 180
206 catccactca aagctgagct cagggtaatg gctgaggggc gagaactgat cctggacctg 240
207 gagaagaatg agcaactttt tgctccttcc tacacagaaa ccattatac ttcaagtgg 300

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210 gtgagcagca acctcagcta cgtcatcgag cccctccctg acagcaaggg ccaacacctt 480
211 atttacagat ctgaacatct caagccgccc ccgggaaact gtgggttcga gcactccaag 540
212 cccaccacca gggactgggc tottcagttt acacaacaga ccaagaagcg acctcgcagg 600
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250 <210> SEQ ID NO: 4

251 <211> LENGTH: 918

252 <212> TYPE: PRT

253 <213> ORGANISM: homo sapiens

255 <400> SEQUENCE: 4

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258 Leu Gln Pro Leu Arg Pro Arg Ala Ala Arg Glu Pro Gly Trp Thr Arg

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date